

In the Claims

Applicant has submitted a new complete claim set showing marked up claims with insertions indicated by underlining and deletions indicated by strikeouts.

Please cancel claims 11-19, 21-24, 28 and 30-47 without prejudice or disclaimer.

Please amend pending claims 1-10, 20, 25-27 and 29 as noted below.

1. (Currently Amended) A method for identifying at least one human gene, including mutated or polymorphic variants thereof, which is associated with a mood disorder or related disorder, comprising:

identifying positions of coding regions/genes in Use of an 8.9 cM region of human chromosome 18q disposed between polymorphic markers D18S68 and D18S979 or a fragment thereof that can be compared to the equivalent regions of DNA from a person afflicted with a mood disorder or a related disorder, and for identifying at least one human gene, including mutated or polymorphic variants thereof, which is associated with a mood disorder or related disorder.

detecting differences between the coding regions/genes of the 8.9 cM region of human chromosome 18q disposed between polymorphic markers D18S68 and D18S979 or a fragment thereof and equivalent regions in the DNA of an individual afflicted with a mood disorder or related disorder, wherein a difference in the coding regions/genes is an indication that the coding region/gene or mutated or polymorphic variant thereof is associated with the mood disorder or related disorder.

2. (Currently Amended) A method for identifying at least one human gene, including mutated or polymorphic variants thereof, which is associated with a mood disorder or related disorder, comprising:

identifying positions of coding regions/genes in Use of a YAC clone comprising a portion of human chromosome 18q disposed between polymorphic markers D18S60 and D18S61 that can be compared to the equivalent regions of DNA from a person afflicted with a mood disorder or a related disorder, and for identifying at least one human gene, including

~~mutated or polymorphic variants thereof, which is associated with a mood disorder or related disorder.~~

detecting differences between the coding regions/genes of the YAC clone comprising a portion of human chromosome 18q disposed between polymorphic markers D18S60 and D18S61 and equivalent regions in the DNA of an individual afflicted with a mood disorder or related disorder, wherein a difference in the coding regions/genes is an indication that the coding region/gene or mutated or polymorphic variant thereof is associated with the mood disorder or related disorder.

3. (Currently Amended) The method of use as claimed in claim 2 wherein said portion comprises the region of chromosome 18q between polymorphic markers D18S68 and D18S979 or a fragment of said region.

4. (Currently Amended) The method of use as claimed in claim 2 wherein said YAC clone is 961_h_9, 942_c_3, 766_f_12, 731_c_7, 907_e_1, 752-g-8 or 717_d_3.

5. (Currently Amended) The method of use as claimed in claim 4 wherein said YAC clone is 961_h_9, 766_f_12 or 907_e_1.

6. (Currently Amended) The method of use as claimed in claim 1 wherein said mood disorder or related disorder is selected from the group consisting of: Diagnostic and Statistical Manual of Mental Disorders, version 4 (DSM-IV) taxonomy and includes mood disorders (296.XX, 300.4, 311, 301, 13, 295.70), schizophrenia and related disorders (295, 297.1, 298.9, 297.3, 298.9), anxiety disorders (300.XX, 309.81, 308.3), adjustment disorders (309, XX) and personality disorders (eodes 301. XX).

7. (Currently Amended) A method of identifying at least one human gene, including mutated or polymorphic variants thereof, which is associated with a mood disorder or related disorder which comprises:

detecting nucleotide triplet repeats in a region of human chromosome 18q disposed between polymorphic markers D18S68 and D18S979, wherein the presence of nucleotide triplet repeats in a region of human chromosome 18q disposed between polymorphic markers D18S68 and D18S979 indicates the presence of a human gene, including mutated or polymorphic variants thereof, which is associated with a mood disorder or related disorder.

8. (Currently Amended) A method of identifying at least one human gene, including mutated or polymorphic variants thereof, which is associated with a mood disorder or related disorder comprising: which comprises fragmentation of a YAC clone as defined in claim 2 and detection of nucleotide triplet repeats;

transforming a YAC clone with a linearized YAC fragmentation vector containing triplet repeats,

identifying a transformed YAC clone containing triplet repeats,

determining a sequence flanking the triplet repeats, and

comparing the sequence to an equivalent region of DNA from a person afflicted with a mood disorder or a related disorder, wherein a difference in the sequence flanking the triplet repeats and the DNA from the afflicted person is an indication of a human gene or mutated or polymorphic variant thereof that is associated with the mood disorder or related disorder.

9. (Currently Amended) A method as claimed in claim 7 wherein said repeated triplet repeat is CAG or CTG.

10. (Currently Amended) A method as claimed in claim 9 wherein said repeated triplet repeat is detected by means of a probe comprising at least 5 CTG and/or CAG repeats.

11-19. (Cancelled)

20. (Currently Amended) Use of a probe of at least 14 contiguous nucleotides of the eDNA of claim 19 or the complement thereof in a A method for detection in a patient of a

pathological mutation or genetic variation associated with a mood disorder or related disorder,
~~which method comprises comprising:~~

hybridizing said a probe of at least 14 contiguous nucleotides of a cDNA obtained by the method of claim 7 with a DNA sample from said patient and a DNA sample from a control individual, wherein the cDNA encodes a human protein which if defective is associated with a mood disorder or related disorder and is the expression product of a human gene, including mutated or polymorphic variants thereof, that is associated with a mood disorder or related disorder, and

comparing the hybridization of the probe to the said patient sample with the hybridization of the probe in the control sample, wherein a difference in the hybridization of the probe in the patient indicates a pathological mutation or genetic variation associated with a mood disorder or related disorder.

21-24. (Cancelled)

25. (Currently Amended) A method of determining the susceptibility of an individual to a mood disorder or related disorder which method comprises ~~analysing a sample of DNA from that individual for the presence of a DNA polymorphism associated with a mood disorder or related disorder in a region of chromosome 18q disposed between polymorphic markers D18S68 and D18S979~~

- a) obtaining a DNA sample from said individual;
- b) providing primers suitable for the amplification of a nucleotide sequence comprised in the sequences shown in Figure 15a, (SEQ ID NO:12) said primers flanking the trinucleotide repeats comprised in said sequences;
- c) applying said primers to the DNA sample and carrying out an amplification reaction;
- d) applying said primers to a DNA sample from a control individual and carrying out the amplification reaction; and
- e) comparing the results of the amplification reaction for the individual and for the control individual;

wherein the presence of an amplified product that includes a DNA polymorphism associated with a mood disorder or related disorder in a region of chromosome 18q disposed between polymorphic markers D18S68 and D18S979 in the individual sample is an indication of the presence of a susceptibility to a mood disorder or related disorder of said individual.

26. (Currently Amended) A method as in claim claims 25 wherein said DNA polymorphism is a trinucleotide repeat expansion.

27. (Currently Amended) A method as in claim 26 wherein said trinucleotide repeat expansion is comprised in a sequence of nucleotides that differ from the sequence of nucleotides shown in any one of figures figure 15a, (SEQ ID NO:12) 16a, 17a or 18a only in said trinucleotide repeat expansion.

28. (Cancelled)

29. (Currently Amended) A method as in claim 25 28 wherein said nucleotide sequence to be amplified is comprised in the sequence shown in Figure 15a (SEQ ID NO:12) and said primers have the sequences shown in Figure 15b (SEQ ID NOs:13 and 14).

30-47. (Cancelled)